Development and applications of GeoChip 3.0 for analysis of microbial community structures, compositions, and potential functions

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Abstract: Functional gene arrays (FGAs), or GeoChip constructed with key genes involved in various biological and geochemical processes have been widely used to analyze microbial communities. Based on GeoChip 2.0, a new generation of GeoChip (GeoChip 3.0) has been developed. GeoChip 3.0 has several new features in terms of coverage, design, and data analysis. GeoChip 3.0 covers approximately 50,000 gene sequences for 306 gene families, and especially functional genes involved in antibiotic resistance and energy metabolism, and phylogenic marker GyrB have been added, which allows us to obtain more information about microbial communities and analyze more diverse environmental samples. For probe design, sequence-specific, exclusive group-specific, inclusive group-specific, and quasi-group probes with different specificities were selected, and all those probes together greatly increase the gene coverage. For data analysis, three strategies have been implemented. First, a universal standard has been implemented so that data normalization and comparison of samples from different sites, time points, or laboratories can be conducted. Second, a genomic standard is used to quantitatively analyze gene abundance. Third, a software package (including databases) has been developed for sequence retrieval, probe design, information storage, and especially, data analysis and automatic update, which greatly facilitate the management and analysis of complicated GeoChip data sets. GeoChip 3.0 has been used for analyses of responses of microbial communities to elevated CO_2 and increased temperature. The results showed that autotrophic CO_2 and N_2 fixation by microorganisms increased significantly in response to elevated CO_2. This also demonstrates that GeoChip can provide insights into biogeochemical processes and functional activities of microbial communities important to human health, agriculture, energy, global climate change, ecosystem management, and environmental cleanup and restoration. It is also particularly useful for providing direct linkages of microbial genes/populations to ecosystem processes and functions.

Keyword (Complete): microarray ; functional gene ; microbial community